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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/092,264

DATE: 03/27/2002
TIME: 14:19:34

Input Set : A:\DC-187.txt
Output Set: N:\CRF3\03272002\J092264.raw

3 <110> APPLICANT: Trustees of Dartmouth College
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES
IN BACTERIA

7 <130> FILE REFERENCE: DC-0188
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/092,264
C--> 9 <141> CURRENT FILING DATE: 2002-03-06

9 <150> PRIOR APPLICATION NUMBER: US 60/273,791
10 <151> PRIOR FILING DATE: 2001-03-06
12 <150> PRIOR APPLICATION NUMBER: US 60/312,546
13 <151> PRIOR FILING DATE: 2001-08-15
15 <150> PRIOR APPLICATION NUMBER: US 60/329,140
16 <151> PRIOR FILING DATE: 2001-10-12

18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 444

24 <212> TYPE: DNA
25 <213> ORGANISM: Staphylococcus aureus
27 <220> FEATURE:

28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(444)
30 <223> OTHER INFORMATION:

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35 Met Ser Asp Gln His Asn Leu Lys Glu Gln Leu Cys Phe Ser Leu Tyr
36 1 5 10 15
38 aat gct caa aga caa gtt aat cgc tac tac tct aac aaa gtt ttt aag 96
39 Asn Ala Gln Arg Gln Val Asn Arg Tyr Tyr Ser Asn Lys Val Phe Lys
40 20 25 30
42 aag tac aat cta aca tac cca caa ttt ctt gtc tta aca att tta tgg 144
43 Lys Tyr Asn Leu Thr Tyr Pro Gln Phe Leu Val Leu Thr Ile Leu Trp
44 35 40 45
46 gat gaa tct cct gta aac gtc aag aaa gtc gta act gaa tta gca ctc 192
47 Asp Glu Ser Pro Val Asn Val Lys Lys Val Val Thr Glu Leu Ala Leu
48 50 55 60
50 gat act ggt aca gta tca cca tta tta aaa cga atg gaa caa gta gac 240
51 Asp Thr Gly Thr Val Ser Pro Leu Leu Lys Arg Met Glu Gln Val Asp
52 65 70 75 80
54 tta att aag cgt gaa cgt tcc gaa gtc gat caa cgt gaa gta ttt att 288
55 Leu Ile Lys Arg Glu Arg Ser Glu Val Asp Gln Arg Glu Val Phe Ile
56 85 90 95
58 cac ttg act gac aaa agt gaa act att aga cca gaa tta agt aat gca 336
59 His Leu Thr Asp Lys Ser Glu Thr Ile Arg Pro Glu Leu Ser Asn Ala
60 100 105 110

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62 tct gac aaa gtc gct tca gct tct tct tta tcg caa gat gaa gtt aaa      384
63 Ser Asp Lys Val Ala Ser Ala Ser Ser Leu Ser Gln Asp Glu Val Lys
64      115      120      125
66 gaa ctt aat cgc tta tta ggt aaa gtc att cat gca ttt gat gaa aca      432
67 Glu Leu Asn Arg Leu Leu Gly Lys Val Ile His Ala Phe Asp Glu Thr
68      130      135      140
70 aag gaa aaa taa      444
71 Lys Glu Lys
72 145
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 147
77 <212> TYPE: PRT
78 <213> ORGANISM: Staphylococcus aureus
80 <400> SEQUENCE: 2
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83 1      5      10      15
86 Asn Ala Gln Arg Gln Val Asn Arg Tyr Tyr Ser Asn Lys Val Phe Lys
87      20      25      30
90 Lys Tyr Asn Leu Thr Tyr Pro Gln Phe Leu Val Leu Thr Ile Leu Trp
91      35      40      45
94 Asp Glu Ser Pro Val Asn Val Lys Lys Val Val Thr Glu Leu Ala Leu
95      50      55      60
98 Asp Thr Gly Thr Val Ser Pro Leu Leu Lys Arg Met Glu Gln Val Asp
99 65      70      75      80
102 Leu Ile Lys Arg Glu Arg Ser Glu Val Asp Gln Arg Glu Val Phe Ile
103      85      90      95
106 His Leu Thr Asp Lys Ser Glu Thr Ile Arg Pro Glu Leu Ser Asn Ala
107      100      105      110
110 Ser Asp Lys Val Ala Ser Ala Ser Ser Leu Ser Gln Asp Glu Val Lys
111      115      120      125
114 Glu Leu Asn Arg Leu Leu Gly Lys Val Ile His Ala Phe Asp Glu Thr
115      130      135      140
118 Lys Glu Lys
119 145
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124 <212> TYPE: DNA
125 <213> ORGANISM: Staphylococcus aureus
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128 <221> NAME/KEY: CDS
129 <222> LOCATION: (1)..(402)
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136 1      5      10      15
138 aat gct caa aga caa gtt aat cgc tac tac tct aac aaa gtt ttt aag      96
139 Asn Ala Gln Arg Gln Val Asn Arg Tyr Tyr Ser Asn Lys Val Phe Lys
140      20      25      30

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142 aag tac aat cta aca tac cca caa ttt ctt gtc tta aca att tta tgg      144
143 Lys Tyr Asn Leu Thr Tyr Pro Gln Phe Leu Val Leu Thr Ile Leu Trp
144      35      40      45
146 gat gaa tct cct gta aac gtc aag aaa gtc gta act gaa tta gca ctc      192
147 Asp Glu Ser Pro Val Asn Val Lys Lys Val Val Thr Glu Leu Ala Leu
148      50      55      60
150 gat act ggt aca gta tca cca tta tta aaa cga atg gaa caa gta gac      240
151 Asp Thr Gly Thr Val Ser Pro Leu Leu Lys Arg Met Glu Gln Val Asp
152 65      70      75      80
154 tta att aag cgt gaa cgt tcc gaa gtc gat caa cgt gaa gta ttt att      288
155 Leu Ile Lys Arg Glu Arg Ser Glu Val Asp Gln Arg Glu Val Phe Ile
156      85      90      95
158 cac ttg act gac aaa agt gaa act att aga cca gaa tta agt aat gca      336
159 His Leu Thr Asp Lys Ser Glu Thr Ile Arg Pro Glu Leu Ser Asn Ala
160      100      105      110
162 tct gac aaa gtc gct tca gct tct tta tct caa gat gaa gtt aaa      384
163 Ser Asp Lys Val Ala Ser Ala Ser Ser Leu Ser Gln Asp Glu Val Lys
164      115      120      125
166 gaa ctt aat cgc tta tta      402
167 Glu Leu Asn Arg Leu Leu
168      130
171 <210> SEQ ID NO: 4
172 <211> LENGTH: 134
173 <212> TYPE: PRT
174 <213> ORGANISM: Staphylococcus aureus
176 <400> SEQUENCE: 4
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183      20      25      30
186 Lys Tyr Asn Leu Thr Tyr Pro Gln Phe Leu Val Leu Thr Ile Leu Trp
187      35      40      45
190 Asp Glu Ser Pro Val Asn Val Lys Lys Val Val Thr Glu Leu Ala Leu
191      50      55      60
194 Asp Thr Gly Thr Val Ser Pro Leu Leu Lys Arg Met Glu Gln Val Asp
195 65      70      75      80
198 Leu Ile Lys Arg Glu Arg Ser Glu Val Asp Gln Arg Glu Val Phe Ile
199      85      90      95
202 His Leu Thr Asp Lys Ser Glu Thr Ile Arg Pro Glu Leu Ser Asn Ala
203      100      105      110
206 Ser Asp Lys Val Ala Ser Ala Ser Ser Leu Ser Gln Asp Glu Val Lys
207      115      120      125
210 Glu Leu Asn Arg Leu Leu
211      130

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date